

GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

Run on: April 19, 2006, 21:51:30 : Search time 260 Seconds
(without alignments)
818.622 Million cell updates/sec

Title: US-09-762-577B-11

Perfect score: 1246
Sequence: 1 cggcacagatctgtgcggg.....agtggtttccctggaggt 1246

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888788028 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cggn_6/prodata/1/ina/1 COMB. seq: *
2: /cggn_6/ptodata/1/ina/5 COMB. seq: *
3: /cggn_6/ptodata/1/ina/6A COMB. seq: *
4: /cggn_6/ptodata/1/ina/6B COMB. seq: *
5: /cggn_6/ptodata/1/ina/H COMB. seq: *
6: /cggn_6/ptodata/1/ina/PCTUS COMB. seq: *
7: /cggn_6/prodata/1/ina/PP COMB. seq: *
8: /cggn_6/ptodata/1/ina/RB COMB. seq: *
9: /cggn_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	#	Query	Match Length	DB	ID	Description
1	1226.4	98.4	1260	3	US-09-949-016-1949	Sequence 1949, Appl
2	1162.4	93.3	1337	3	US-09-127-928-1	Sequence 1, Appl
3	492.4	39.5	8572	3	US-09-949-016-13691	Sequence 13691, A
4	224	18.0	2226	3	US-09-023-655-334	Sequence 334, Appl
5	204.4	16.4	601	3	US-09-949-016-66130	Sequence 66130, A
6	175.2	14.1	601	3	US-09-949-016-66140	Sequence 66140, A
7	147.2	11.8	601	3	US-09-949-016-66139	Sequence 66139, A
8	135	10.8	200	3	US-09-164-216	Sequence 216, Appl
9	135	10.8	200	3	US-09-023-655-387	Sequence 387, Appl
10	111.2	8.9	601	3	US-09-949-016-66134	Sequence 66134, A
11	97	7.8	2450	3	US-09-201-926-39	Sequence 39, Appl
12	97	7.8	2450	3	US-09-001-922-39	Sequence 39, Appl
13	97	7.8	2474	3	US-09-011-356-39	Sequence 39, Appl
14	97	7.8	2474	3	US-09-672-717-226	Sequence 226, Appl
15	97	7.8	2676	3	US-09-212-971-11	Sequence 11, Appl
16	97	7.8	2676	3	US-09-800-949R-11	Sequence 11, Appl
17	97	7.8	2676	3	US-09-617-033A-11	Sequence 11, Appl
18	88.2	7.1	601	3	US-09-949-016-66136	Sequence 66136, A
19	87.2	7.0	601	3	US-09-949-016-66138	Sequence 66138, A
20	87	7.0	601	3	US-09-949-016-66135	Sequence 66135, A
21	86.6	7.0	2862	3	US-08-569-799-13	Sequence 13, Appl
22	86.6	7.0	2862	3	US-09-689-366-13	Sequence 13, Appl
23	86.6	7.0	2862	3	US-10-332-246-13	Sequence 13, Appl
24	86.6	7.0	2862	6	PCT-US96-12860-13	Sequence 13, Appl

ALIGNMENTS

25	86.6	7.0	3151	3	US-09-212-971-13	Sequence 13, Appl
26	86.6	7.0	3151	3	US-08-800-939A-13	Sequence 13, Appl
27	85	6.8	2416	3	US-09-617-936-41	Sequence 41, Appl
28	85	6.8	2416	3	US-09-011-356-41	Sequence 41, Appl
29	85	6.8	2416	3	US-09-672-717-228	Sequence 41, Appl
30	85	6.8	2416	3	US-09-201-932-41	Sequence 41, Appl
31	85	6.8	2416	3	US-09-949-016-66131	Sequence 66131, A
32	83.4	6.7	601	3	PCT-US95-0922A-1	Sequence 1, Appl
33	80.8	6.5	3532	2	US-09-205-204-1	Sequence 1, Appl
34	80.8	6.5	3532	3	US-09-212-971-7	Sequence 7, Appl
35	80.8	6.5	3532	3	US-09-800-929A-7	Sequence 7, Appl
36	80.8	6.5	3732	3	US-09-617-053A-7	Sequence 7, Appl
37	80.8	6.5	2589	3	PCT-US96-12860-1	Sequence 1, Appl
38	80.8	6.5	3532	3	US-09-212-971-7	Sequence 1, Appl
39	80.8	6.5	3732	3	US-09-569-749-1	Sequence 7, Appl
40	80.8	6.5	3732	3	US-09-689-366-1	Sequence 7, Appl
41	80.8	6.5	3732	3	US-09-617-053A-7	Sequence 7, Appl
42	79.6	6.4	1448	3	US-09-579-692B-57	Sequence 57, Appl
43	79.6	6.4	2563	3	US-09-016-434-1076	Sequence 1076, Appl
44	79.6	6.4	2563	3	US-09-023-655-894	Sequence 894, Appl
45	79.6	6.4	2601	3	US-09-569-749-3	Sequence 3, Appl

Db 830 CCAGCCGAGGCCAGAGGGGTCTGGGTTCTGGCCCACAGGCCAGGGAG 889
 Qy 223 AlaglneuargLengLingLingLurgrThCysLysValCysLeuPargAlaVal 242
 Db 890 GGCAGCTGCGCGCGTCAAGGGAGGGAGGGAGGGAGGGAGGGAGGGAG 949
 Qy 243 SerIleValPheValProGlyYHIsleUvaLyCysAlaGluCysAlaProGlyLeuIn 262
 Db 950 TCCATGGCTTCCTGGCTGCGCCACCTGTCGTCGTCGAGTGCTGCCGCG 1009
 Qy 263 LeuCySProIeCySArgAlaProValLrgSeArgValArgThrPheLeu*11a 282
 Db 1010 CTGGCCCATCTGAGCAGGCCCTGCTCCAGCGCGCGAGCTGCTGAG 1069
 Qy 283 ArgQysHsAglYargProGlyYLeuInSerDlyLeuProlaProLeuCysLeuPhe 302
 Db 1070 AGCTGCGATGCGGGCGAGGAGCTGCAAGAGGGCTCCCTCTCCCTGTC 1129
 Qy 303 TyrThrValPhenPhePalaCys 309
 Db 1130 TGGACTGCTTCCTGGCTG 1150

RESULT 3

US-09-949-015-13691
 Sequence 13691, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OR DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows version 4.0
 ; SEQ ID NO: 13691
 ; LENGTH: 8572
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-13691

Alignment Scores:

Pred. No.:	1.27e-77	Length:	8572
Score:	1030.00	Matches:	306
Percent Similarity:	21.7%	Conservative:	1
Best Local Similarity:	21.6%	Mismatches:	2
Query Match:	59.8%	Indels:	1107
DB:	3	Gaps:	6

US-09-762-577B-12 (1-309) x US-09-949-016-13691 (1-8572)

Qy 1 MetGlyProLySAspSerAlaLysVcYsLeuLhLArgGlyProGlnProSerIstPala 20
 Db 2174 ArgGGACTTAAGAACAGCTGCAGTCAGGCTGCAAGCCAGGCTGCA 2233
 Qy 21 AlaGlyLysArgProThrGlnGluArgCysGlyProAspSerIleGlySerProValu 40
 Db 2234 GCGGGAATGATGCCACGGAGGGCTTACAATACTGGCACAGCCAT 2293
 Qy 41 GlyLeuAspThrQsAlaTrpAspHisValAspGlyGlnIleLeuGlyLysLeu 60
 Db 2294 GacCTGGAACACCTGGACAGCTGGACACGCTGGATGCTGGCGAGCG 2353
 Qy 61 ProLeuThrLugLugLugLugLugLugLysAlaGlyAlaThrLeuSerGlyProAla 80
 Db 2354 CCCTGacAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2413

Qy 81 PheProGlyMarGlySerGluGluLeuArgLeuAlaSerPheTyxAspTPPProLeuThr 100
 Db 2414 TCCCCCGCATGGCTCTGAGGAGTCGTCGTCGCTCTCTAAGCTGAGCCGCTRACT 2473
 Qy 101 AlaglvalProProgluLeuLeuAlaAlaAlaAlaAlaAlaAlaLgylPhePheHistR 116
 Db 2474 GCTGAGGCGCCACCCGAGCTCTGCGCTGCGGCTCTTCACAC-AGGTCAGTCCG 2532
 Qy 116 ----- 116
 Db 2533 GCGGAGGGGGCTTCCGGCCCTGGGAGCTGGCACCTTCAGCCAGGGC 2592
 Qy 116 ----- 116
 Db 2593 TCTGCCTCTCGTAGATCCATCCCCCARAGGAAGGGCTGGCTGACACCCCTCCGGAGCAG 2652
 Qy 116 ----- 116
 Db 2653 TGGTCMGCAGGCCCTCCAGTGCCCTGGCTGAGCTGACACCCCTCCGGAGCT 2712
 Qy 116 ----- 116
 Db 2713 CTTGCTGCTGAGTGTCTAGACCGTGGACCTGCTGACCTCTGGCACAGCT 2772
 Qy 116 ----- 116
 Db 2773 GAGGGCTCAGCTGTGGAGGCCACCTGGTACAGTACCCCTTGTGATAGAGT 2832
 Qy 116 ----- 116
 Db 2833 GGGTGGGCTGACATTCCTGGGGCCACCTTCCCCTGCTGTTCTGACAGGGAGA 2892
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 Db 2893 GCGAGATCTTAAAGAACAGGAATCGGGTACGGTACGGAAAGGGAGGTC 2952
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 Db 2953 CTGGATCTCAGCTGTTGGGAATTCTCCAGGCCCCAACCTGCACTACTGCTGCT 3012
 Qy 116 ----- 116
 Db 3013 TCCCCACTGATCAGTCCGGGAGTACCTATCCCTGACTCTAGTCTGCCCCGGCTCTC 3072
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 Db 3073 TCCCTCTACAGCTGAGGCCATGCTGAGCTGACTCTAGTCTGCCCCGGCTCTC 3132
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 Db 3133 CTGGCTTAAGGACAGGGCAGGAGGGCCACCGAGGGCTTACAATACTGGCACAGCCAT 3192
 Qy 116 ----- 116
 Db 3193 GTCTATGTCAGCTGGCTGCTGGGGGCCACCTCTGGTAAGGCTGGACCACTAA 3252
 Qy 116 ----- 116
 Db 3253 GACAGCTGGCTGGGGGAGCACTGGCTGGACAGTCAGAAGCCGGTGGGGAGG 3312
 Qy 116 ----- 116
 Db 3313 CCCAGCTCACCAACCTCTGGAAAGTCACAGGCTCTGGAGGCAAAGGCCAGGGC 3372
 Qy 116 ----- 116
 Db 3373 ATGGCAGGTGGAGGCCGGGCTTCTGGGCTGGTAAAGGCTGGCTGCCCCATGCAAGCC 3432
 Qy 116 ----- 116
 Db 3433 AACCTGAGTCAGTGGAGGAGCTGAGTATGCAATGAGATCCGATGAGGGAGGGTC 3492
 Qy 116 ----- 116